STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/530,844
Source: PCT
Date Processed by STIC: 4-19-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/530,844

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .5; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.

8 Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.821 of Sequence Rules, use of <220> - <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213> Response — Per 1.821 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220> - <223> section is required when <213> response is Unknown or Artificial Sequence.

11 ✓ Use of <220> —

Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol 63, No 104, pp 29631-32) (See 1.821 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003

PCT

RAW SEQUENCE LISTING DATE: 04/19/2005
PATENT APPLICATION: **US/10/530,844** TIME: 08:46:17

Input Set : **A:\PTO.SR.txt**
Output Set: **N:\CRF4\04192005\J530844.raw**

```
 5 <110> APPLICANT: Consortium for elektrochemische Industrie GmbH
 9 <120> TITLE OF INVENTION: Feedback resistente Homoserin-Transsuccinylasen mit
11       modifiziertem C-Terminus
15 <130> FILE REFERENCE: Co10221
C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/530,844
C--> 20 <141> CURRENT FILING DATE: 2005-04-08
24 <160> NUMBER OF SEQ ID NOS: 12
28 <170> SOFTWARE: PatentIn Ver. 2.0
32 <210> SEQ ID NO: 1
34 <211> LENGTH: 930
36 <212> TYPE: DNA
38 <213> ORGANISM: Escherichia coli
42 <220> FEATURE:
44 <221> NAME/KEY: CDS
46 <222> LOCATION: (1)..(930)
50 <300> PUBLICATION INFORMATION:
52 <301> AUTHORs: Blattner, F. R.
54 <302> TITLE: The complete genome sequence of Escherichia coli K-12.
56 <303> JOURNAL: Science
58 <304> VOLUME: 277
60 <305> ISSUE: 533
62 <306> PAGES: 1453-1474
64 <307> DATE: 1997
66 <308> DATABASE ACCESSION NO: Blattner, F.R.
W--> 70 <309> PUBLICATION INFORMATION: I
72 atg ccg att cgt gtg ccg gac gag cta ccc gcc gtc aat ttc ttg cgt   48
74 Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg
76   1               5                  10                  15
80 gaa gaa aac gtc ttt gtg atg aca act tct cgt gcg tct ggt cag gaa   96
82 Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu
84              20                  25                  30
88 att cgt cca ctt aag gtt ctg atc ctt aac ctg atg ccg aag aag att   144
90 Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile
92          35                  40                  45
96 gaa act gaa aat cag ttt ctg cgc ctg ctt tca aac tca cct ttg cag   192
98 Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln
100      50                  55                  60
104 gtc gat att cag ctg ttg cgc atc gat tcc cgt gaa tcg cgc aac acg   240
106 Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr
108  65                  70                  75                  80
112 ccc gca gag cat ctg aac aac ttc tac tgt aac ttt gaa gat att cag   288
114 Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln
116                 85                  90                  95
```

pls do NOT use foreign language in U.S. Applications.
Does Not Comply
Corrected Diskette Needed
(pg. 1-5)

Mandatory, if <308> is shown, then <309> must be inserted.

RAW SEQUENCE LISTING DATE: 04/19/2005
PATENT APPLICATION: US/10/530,844 TIME: 08:46:17

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\04192005\J530844.raw

```
120 gat cag aac ttt gac ggt ttg att gta act ggt gcg ccg ctg ggc ctg   336
122 Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu
124             100                 105                 110
128 gtg gag ttt aat gat gtc gct tac tgg ccg cag atc aaa cag gtg ctg   384
130 Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu
132         115                 120                 125
136 gag tgg tcg aaa gat cac gtc acc tcg acg ctg ttt gtc tgc tgg gcg   432
138 Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala
140     130                 135                 140
144 gta cag gcc gcg ctc aat atc ctc tac ggc att cct aag caa act cgc   480
146 Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg
148 145                 150                 155                 160
152 acc gaa aaa ctc tct ggc gtt tac gag cat cat att ctc cat cct cat   528
154 Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His
156                 165                 170                 175
160 gcg ctt ctg acg cgt ggc ttt gat gat tca ttc ctg gca ccg cat tcg   576
162 Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser
164             180                 185                 190
168 cgc tat gct gac ttt ccg gca gcg ttg att cgt gat tac acc gat ctg   624
170 Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu
172         195                 200                 205
176 gaa att ctg gca gag acg gaa gaa ggg gat gca tat ctg ttt gcc agt   672
178 Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser
180     210                 215                 220
184 aaa gat aag cgc att gcc ttt gtg acg ggc cat ccc gaa tat gat gcg   720
186 Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala
188 225                 230                 235                 240
192 caa acg ctg gcg cag gaa ttt ttc cgc gat gtg gaa gcc gga cta gac   768
194 Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp
196                 245                 250                 255
200 ccg gat gta ccg tat aac tat ttc ccg cac aat gat ccg caa aat aca   816
202 Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr
204             260                 265                 270
208 ccg cga gcg agc tgg cgt agt cac ggt aat tta ctg ttt acc aac tgg   864
210 Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp
212         275                 280                 285
216 ctc aac tat tac gtc tac cag atc acg cca tac gat cta cgg cac atg   912
218 Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met
220     290                 295                 300
224 aat cca acg ctg gat taa                                         930
226 Asn Pro Thr Leu Asp
W--> 228 305                 310
234 <210> SEQ ID NO: 2
236 <211> LENGTH: 309
238 <212> TYPE: PRT
240 <213> ORGANISM: Escherichia coli
244 <400> SEQUENCE: 2
246 Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg
248   1               5                  10                  15
```

delete

RAW SEQUENCE LISTING DATE: 04/19/2005
PATENT APPLICATION: US/10/530,844 TIME: 08:46:17

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\04192005\J530844.raw

```
252 Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu
254              20                  25                  30
258 Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile
260          35                  40                  45
264 Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln
266      50                  55                  60
270 Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr
272  65                  70                  75                  80
276 Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln
278                  85                  90                  95
282 Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu
284              100                 105                 110
288 Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu
290          115                 120                 125
294 Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala
296      130                 135                 140
300 Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg
302 145                 150                 155                 160
306 Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His
308                 165                 170                 175
312 Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser
314              180                 185                 190
318 Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu
320          195                 200                 205
324 Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser
326      210                 215                 220
330 Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala
332 225                 230                 235                 240
336 Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp
338                 245                 250                 255
342 Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr
344              260                 265                 270
348 Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp
350          275                 280                 285
354 Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met
356      290                 295                 300
360 Asn Pro Thr Leu Asp
362 305
368 <210> SEQ ID NO: 3
370 <211> LENGTH: 34
372 <212> TYPE: DNA
374 <213> ORGANISM: Artificial Sequence
378 <220> FEATURE:
380 <223> OTHER INFORMATION: Description of Artificial Sequence:
382       Oligonucleotide metAde11
386 <400> SEQUENCE: 3
388 ctatttgtta gtgaataata gtactgagct ctgg                              34
394 <210> SEQ ID NO: 4
396 <211> LENGTH: 34
```

What is this?

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Input Set : **A:\PTO.SR.txt**
Output Set: **N:\CRF4\04192005\J530844.raw**

398 <212> TYPE: DNA
400 <213> ORGANISM: Artificial Sequence
404 <220> FEATURE:
406 <223> OTHER INFORMATION: Description of Artificial Sequence:
408 Oligonucleotide metAdel2
412 <400> SEQUENCE: 4
414 ctggtggata tatgagatct ggtagacgta atag 34
420 <210> SEQ ID NO: 5
422 <211> LENGTH: 33
424 <212> TYPE: DNA
426 <213> ORGANISM: Artificial Sequence
430 <220> FEATURE:
432 <223> OTHER INFORMATION: Description of Artificial Sequence:
434 Oligonucleotide metAext1
438 <400> SEQUENCE: 5
440 tggtggatat atgagatctg gtagacgtaa tag 33
446 <210> SEQ ID NO: 6
448 <211> LENGTH: 34
450 <212> TYPE: DNA
452 <213> ORGANISM: Artificial Sequence
456 <220> FEATURE:
458 <223> OTHER INFORMATION: Description of Artificial Sequence:
460 Oligonucleotide metAext2
464 <400> SEQUENCE: 6
466 gtatttgtta gtgaataata gtactgagct ctgg 34
472 <210> SEQ ID NO: 7
474 <211> LENGTH: 33
476 <212> TYPE: DNA
478 <213> ORGANISM: Artificial Sequence
482 <220> FEATURE:
484 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial Gene
486 Sequence
490 <400> SEQUENCE: 7
492 tcatatatcc accagctatt tgttagtgaa taa 33
498 <210> SEQ ID NO: 8
500 <211> LENGTH: 10
502 <212> TYPE: PRT
504 <213> ORGANISM: Artificial Sequence
508 <220> FEATURE:
510 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial
512 Protein Sequence
516 <400> SEQUENCE: 8
518 Ser Tyr Ile His Gln Leu Phe Val Ser Glu
520 1 5 10
526 <210> SEQ ID NO: 9
528 <211> LENGTH: 102
530 <212> TYPE: DNA
532 <213> ORGANISM: Artificial Sequence
536 <220> FEATURE:

Same errors

What is the source of genetic material?

Invalid response

What is the source of genetic material?

Invalid response

↑ See item # 11 on error Summary Sheet.

RAW SEQUENCE LISTING DATE: 04/19/2005
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Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\04192005\J530844.raw

√ SAME errors

538 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial Gene
540 Sequence
544 <400> SEQUENCE: 9
546 tcatatatcc accactattt gttagtgaat aatagtactg agctctggat gcatacgcgt 60
550 ttaattaagc ggccgcactg cgatgagtgg cagggcgggg cg 102
556 <210> SEQ ID NO: 10
558 <211> LENGTH: 34
560 <212> TYPE: PRT
562 <213> ORGANISM: Artificial Sequence
566 <220> FEATURE:
568 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial
570 Protein Sequence
574 <400> SEQUENCE: 10
576 Ser Tyr Ile His His Tyr Leu Leu Val Asn Asn Ser Thr Glu Leu Trp
578 1 5 10 15
582 Met His Thr Arg Leu Ile Lys Arg Pro His Cys Asp Glu Trp Gln Gly
584 20 25 30
588 Gly Ala
596 <210> SEQ ID NO: 11
598 <211> LENGTH: 102
600 <212> TYPE: DNA
602 <213> ORGANISM: Artificial Sequence
606 <220> FEATURE:
608 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial Gene
610 Sequence
614 <400> SEQUENCE: 11
616 tcatatatcc accagtattt gttagtgaat aatagtactg agctctggat gcatacgcgt 60
620 ttaattaagc ggccgcactg cgatgagtgg cagggcgggg cg 102
626 <210> SEQ ID NO: 12
628 <211> LENGTH: 34
630 <212> TYPE: PRT
632 <213> ORGANISM: Artificial Sequence
636 <220> FEATURE:
638 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial
640 Protein Sequence
644 <400> SEQUENCE: 12
646 Ser Tyr Ile His Gln Tyr Leu Leu Val Asn Asn Ser Thr Glu Leu Trp
648 1 5 10 15
652 Met His Thr Arg Leu Ile Lys Arg Pro His Cys Asp Glu Trp Gln Gly
654 20 25 30
658 Gly Ala

↑ See item #11 on error Summary Sheet.

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/19/2005
PATENT APPLICATION: **US/10/530,844** TIME: 08:46:18

Input Set : **A:\PTO.SR.txt**
Output Set: **N:\CRF4\04192005\J530844.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1,3,5,7,9,11,13,15,16,18,20,22,24,26,28,30,32,34,36,38,40
Seq#:1; Line(s) 42,44,46,48,50,52,54,56,58,60,62,64,66,68,70,72,74,76,78,80
Seq#:1; Line(s) 82,84,86,88,90,92,94,96,98,100,102,104,106,108,110,112,114
Seq#:1; Line(s) 116,118,120,122,124,126,128,130,132,134,136,138,140,142,144
Seq#:1; Line(s) 146,148,150,152,154,156,158,160,162,164,166,168,170,172,174
Seq#:1; Line(s) 176,178,180,182,184,186,188,190,192,194,196,198,200,202,204
Seq#:1; Line(s) 206,208,210,212,214,216,218,220,222,224,226,228,230,232,234
Seq#:2; Line(s) 236,238,240,242,244,246,248,250,252,254,256,258,260,262,264
Seq#:2; Line(s) 266,268,270,272,274,276,278,280,282,284,286,288,290,292,294
Seq#:2; Line(s) 296,298,300,302,304,306,308,310,312,314,316,318,320,322,324
Seq#:2; Line(s) 326,328,330,332,334,336,338,340,342,344,346,348,350,352,354
Seq#:2; Line(s) 356,358,360,362,364,366,368
Seq#:3; Line(s) 370,372,374,376,378,380,382,384,386,388,390,392,394
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Seq#:11; Line(s) 598,600,602,604,606,608,610,612,614,616,618,620,622,624
Seq#:11; Line(s) 626
Seq#:12; Line(s) 628,630,632,634,636,638,640,642,644,646,648,650,652,654
Seq#:12; Line(s) 656,658,660,662,664,666

VERIFICATION SUMMARY DATE: 04/19/2005
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Input Set : **A:\PTO.SR.txt**
Output Set: **N:\CRF4\04192005\J530844.raw**

L:18 M:270 C: Current Application Number differs, Replaced Application Number
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:70 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:1
L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1